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Thermodynamic thresholds in water/methanol solutions

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Summary. — The non-ideality of water/methanol solutions is established by the interplay between hydrophilic and hydrophobic interactions that take place within the system and determine its physical properties. These interactions have a different energetic dependence on the temperature and the measurement of transport parameters, such as self-diffusion coefficient and relaxation time, allows to obtain important information about that dependence. Here it is shown how thermodynamic parameters such as temperature and concentration determine the character and the physical properties of the solutions. Furthermore, the thermodynamic thresholds that separate the different energetic regions were identified.

1. – Introduction

Aqueous solutions of molecules containing moieties with opposite behaviour with respect to attracting water molecules display a non-linear trend in dynamic and thermodynamic quantities as a function of the concentration. The main interactions taking place within these solutions are the hydrophilic (water-loving, polar) and hydrophobic (water-hating or lipophilic) ones, that compete with each other to determine the properties of the solution and depend on the thermodynamic conditions such as temperature and concentration [1]. The comprehension of the interplay between these interactions within aqueous solutions is very important from different points of views, especially from a biological side. In fact, it is well known that the biological macromolecules and life itself need a minimum amount of water to support their activities [2,3]. However, the complexity of large molecules does not allow an easy modeling and comprehension of the microscopic mechanisms underlying amphiphilic aqueous solutions [4,5].

The simplest molecule, that in solution with water shows both hydrophilic and hydrophobic interactions (*i.e.*, an amphiphile), is methyl alcohol (or methanol) that indeed

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can constitute a model molecule to probe and investigate the properties of these solutions by varying temperature and concentration [6, 7].

One of the earliest observations came from Gibson who in 1935 found a minimum for the compressibility and partial volumes of water/methanol solutions [8]. This behaviour has been explained by hypothesizing that the presence of methanol, unlike other types of solute, favours the association of water molecules. Lately, Frank and Evans in 1945 added that the presence of hydrophobic entities significantly enhances the water structuring causing the formation of more ordered structures near the methyl headgroup [9]. These were firstly interpreted as “iceberg-like” structures, but their existence is still up for discussion [10]. When water is close to hydrophobic moieties, it cannot hydrogen bond with them and its enthalpy increases. In order to compensate for the rise in enthalpy, water molecules rearrange forming low-density water clusters with lower entropy, as happens during the folding of proteins [11]. However, hydration and solvation processes depend on both temperature and concentration, much like entropic and enthalpic mechanisms [12]. In the last years, many experimental and theoretical studies have tried to address the important issue of determining the solution properties at specific thermodynamic conditions [13-21], also for the related industrial applications [22].

Recently, a careful study of the relaxation times going from high (360 K) to very low temperature (160 K) showed opposite thermal behaviors for water/methanol solutions [1]. At the highest temperatures, the thermal energy and van der Waals interaction destabilize the hydrogen bonds and hydrophobic forces determine the properties of the solution. This holds for temperatures higher than 320 K, whereas for lower temperatures the hydrogen bonds progressively increase their strength and lifetime with the development of low-density liquid (LDL) structures down to about $T_L = 225$ K. This temperature has been identified with that of the fragile-to-strong crossover for water below which the tetrahedral network of water is fully developed for aqueous systems with different dimensionality [23]. The crossover temperature corresponds also to the maximum for the correlation length of water molecules that in turn defines the locus of the Widom line, the critical isocore departing from the hypothesized liquid-liquid critical point for water [24, 25]. Within the mentioned study, the dependence of the Widom line on the concentration has been pointed out [1]. Furthermore, by looking at the microscopic mechanisms underlying the different interactions occurring in water/methanol solutions, their competition has been studied by means of Nuclear Magnetic Resonance (NMR) spectroscopy [21].

Here, we will merge the results of both structural and dynamical experiments obtained by using NMR spectroscopy on water/methanol solutions. The aim is the definition of the thermodynamic thresholds that separate different regions corresponding to different structural arrangements and dynamical regimes. We find that only the thermal threshold defining the hydrophilic/hydrophobic competition is slightly dependent on the molar fraction of the solution. On the other hand, the concentration thresholds determining the solution properties seem to soften on cooling.

2. – Methods

Nuclear Magnetic Resonance (NMR) is a very powerful experimental technique allowing the observation of the individual molecular species present in a solution. NMR experiments were performed on water/methanol solutions from ambient temperature to the freezing temperature (of the considered concentration) by spanning the whole range of concentration. For the measurements we used a Bruker Avance spectrometer operating

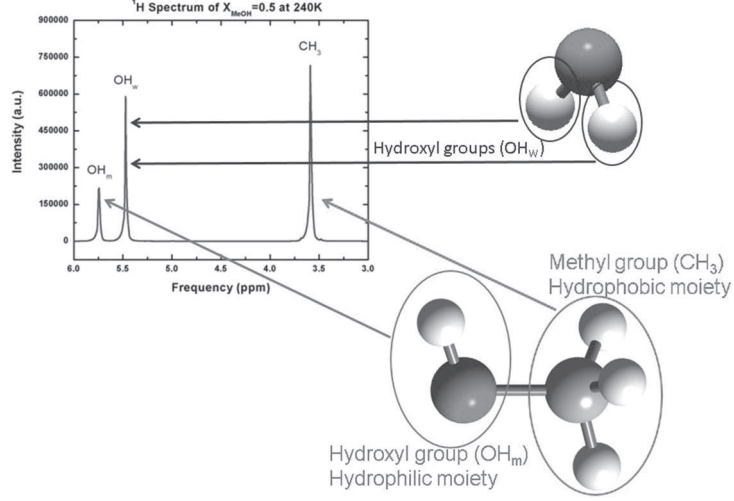


Fig. 1. – The ^1H NMR spectrum of the water/methanol solution for a methanol molar fraction of 0.5 and a temperature of 240 K. Water and methanol molecules, with their protons originating the NMR signal are highlighted.

at 700 MHz (proton resonance frequency) and the experimental details are reported in [6, 18].

In fig. 1 the proton NMR spectrum of the water/methanol solution with methanol molar fraction (X_{MeOH}) equal to 0.5 is reported for $T = 240$ K. The individual assignments of the NMR peaks are indicated by the arrows from the corresponding moiety. Note that each peak is well resolved, furthermore at the equimolar concentration the area below the water hydroxyl protons (OH_w) and methanol methyl protons (CH_3) peaks is respectively double and triple compared to that below the methanol hydroxyl protons (OH_m).

For the investigation of dynamical regimes, we considered the measurement of the self-diffusion coefficient (D_S) and of the relaxation times of the nuclear magnetization (the spin-lattice, T_1 , and spin-spin, T_2) in the whole range of molar fractions down to the lowest temperature of 205 K. D_S was measured by using the Pulsed Gradient Stimulated Echo pulse sequence as described in [18], whereas T_1 and T_2 were evaluated by means of the inversion recovery and spin-echo pulse sequences, respectively [6]. Furthermore, by assuming that both relaxation times can be expressed in terms of the same average correlation time (τ_c), this quantity can be calculated by solving the following equation [21, 26]:

$$(1) \quad 12B(\omega_0\tau_c)^4 + (37B - 8)(\omega_0\tau_c)^2 + 10B - 5 = 0,$$

where B is $T_2/2T_1$ and ω_0 the proton Larmor frequency.

3. – Results and discussion

For what concerns the structural investigations, from the values of the measured chemical shift, δ , we observed that the temperature behavior is not so affected by the concentration. In fact, all the considered molar fractions, going from pure water to

methanol, show essentially the same temperature trend for δ . This means that, even if the local structures within the solution are quite different, as well as for pure water and methanol, the temperature variation has the strongest influence on the studied structure. This is consistent with the theoretical scenarios predicted by the Mode Coupling Theory for the liquid state and glass forming systems and by the Energy Landscape [27-30]. In fact, the higher the temperature, the higher the number of degrees of freedom corresponding to multiple relaxations due to the exploration of the local minima of the Energy Landscape [31]. When the system is cooled down, the number of allowed energy states progressively decreases until only hopping processes between minima of uniform height are permitted [32].

Coming back to water/methanol solutions, the distance between the different NMR peaks varies with temperature and concentration [18]. In particular, the distance between the hydroxyl protons is maximum around the temperature $T_h \sim 290$ K and depends on the methanol molar fraction being largest for $X_{MeOH} \sim 0.45$ [21]. The increase in the distance between the hydroxyl peaks corresponds to a decreasing rate for the chemical exchange because the two molecular species experience different chemical environments. This means that for a larger peaks distance the hydroxyl species are poorly correlated or randomly mixed. However, interesting information about the hydrogen bonding dependence on temperature and concentration can be achieved by looking at the dependence on the molar fraction, at a fixed temperature, of the chemical shift of the water peak. From an inspection of fig. 2 in fact, it is possible to note that the largest slope is observed at the lowest methanol concentration and at the highest temperature. The flattest region is that at intermediate molar fractions and seems to extend at the lowest temperatures where the overall trend would approach an ideal behavior [1].

The chemical shift of water hydroxyl protons increases with the methanol molar fraction due to the increasing shielding effect of methanol methyl groups [18,33]. This effect is more pronounced at high temperature and high water content that is when the hydropho-

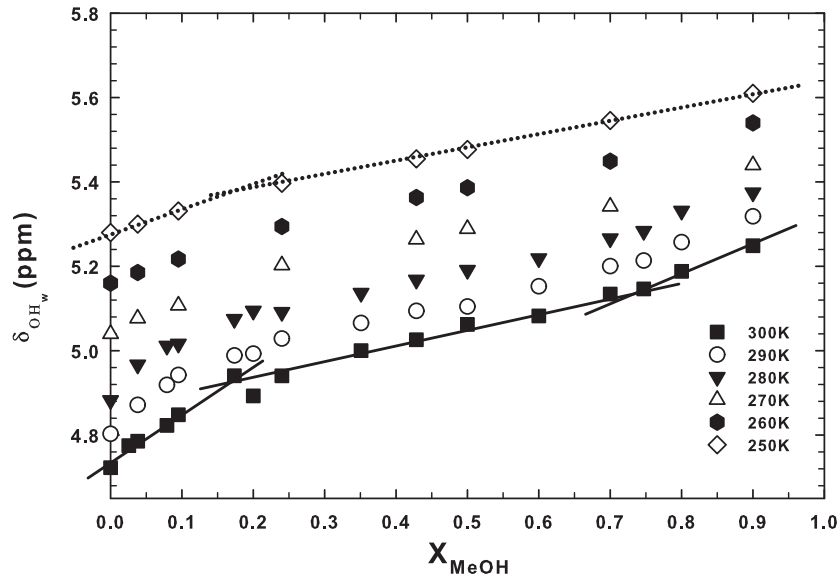


Fig. 2. – The chemical shift of the water peak as a function of the methanol molar fraction at fixed temperatures in the range 250–300 K. Figure adapted from [18].

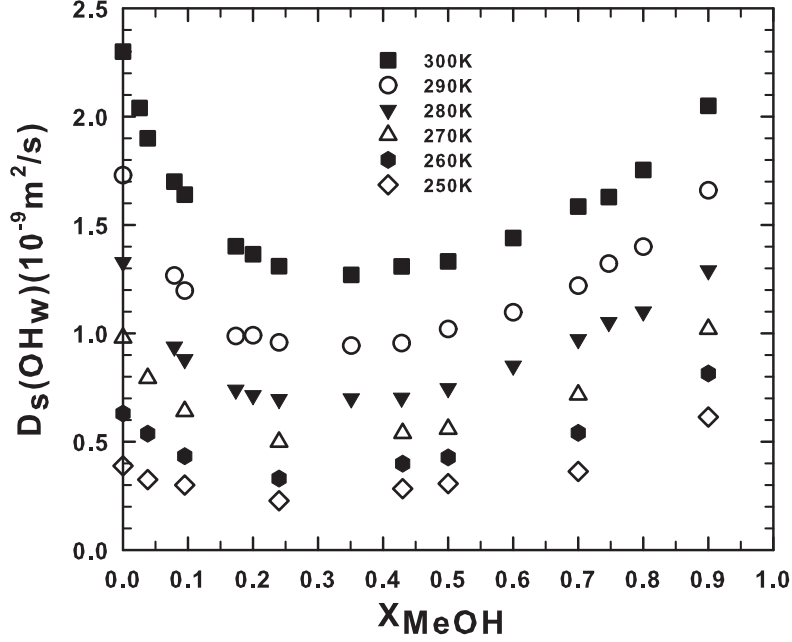


Fig. 3. – The water self-diffusion coefficient, D_S , measured for the same samples (and at the same conditions) reported in fig. 2. Figure adapted from [18].

bic interaction can destabilize hydrogen bonding and may provoke a rearrangement of the water HB network. Thus, for $X_{MeOH} < 0.2$ the solution shows a higher sensitivity to changes in concentration with a subsequent different structural configuration. This happens also, but to a lesser extent, for $X_{MeOH} > 0.7$ when the presence of water molecules provokes a structural rearrangement of chains and rings sub-domains that are characteristic of methanol [20,34]. Finally, the small value of the slope within the intermediate concentration region confirms that mixed and stable clusters form in solution and have a slower dynamics with respect to that in pure liquids [6]. This is testified also by fig. 3 in which we show the water self-diffusion coefficient measured for the same samples (and at the same conditions) reported in fig. 2.

From this figure, it is indeed evident that the dynamics in the solution is slower than that of the pure compounds especially at equimolar condition [6,14,35]. In particular, the occurrence of a minimum is evident for values of methanol molar fractions corresponding to about two to four water molecules per methanol molecule. For $0.7 < X_{MeOH} < 0.2$ the “guest” molecules are solvated within the hosting structures causing a progressive morphological modification. For intermediate values instead, the number of molecules of both substances involved in the formation of long-lived clusters is comparable. The evidence that the minimum is shifted toward the water concentrated region and that its depth decreases with temperature confirms the dominant role of hydrogen bonding.

In a previous work, the relaxation times of the nuclear magnetization were measured in water/methanol solutions as a function of the temperature discriminating the different contribution from all the individual molecular groups [6]. It was found that the spin-lattice relaxation time, T_1 , is shorter for the molecules in the solution than in pure liquids. The hydroxyl protons of methanol are very influenced by water molecules, although

their T_1 equals that of water hydroxyl protons upon cooling down to $T_K = 245$ K for all concentrations. Below this temperature, the thermal behavior of the two relaxation times becomes different implying that the two molecular groups probe the same environment only for temperatures higher than T_K . Concerning the spin-spin relaxation time, T_2 , that of the CH_3 protons in solution decreases sharply until about $T_x = 265$ K after which its thermal behavior starts to resemble those of the hydroxyl groups. Starting from about 300 K, the experimental values of T_2 for both OH_w and OH_m protons, for all concentrations, are about two orders of magnitude lower than those of pure water and methanol and increase by lowering the temperature. On the contrary, T_2 of pure water and methanol decreases with temperature in all the temperature range [6]. The data show that, for temperatures lower than T_K , T_2 for all the molecular group assumes the same behavior of that measured in the pure compounds, indicating that “aggregation” processes are enhanced at high temperature.

From these two relaxation times, we evaluated the average correlation time that is reported in fig. 4 for an equimolar solution for both hydrophilic and hydrophobic moieties [21]. In fact, as already mentioned, since the highest non-linearity (excess) lies approximately at the equimolar value, here the mixed clustering of water and methanol molecules is more enhanced. Moreover, a temperature of about 200 K can be reached without crystallization intervening and thus the water supercooled regime can be explored.

The thermal behaviour of the correlation time for the different moieties has very interesting features. That of hydroxyl protons shows a first change at about 290 K (left panel of fig. 4). This coincides with the temperature beyond which hydrophobicity is able to compete with hydrophilicity. Its onset is instead located at about 265 K where τ_c of methyl

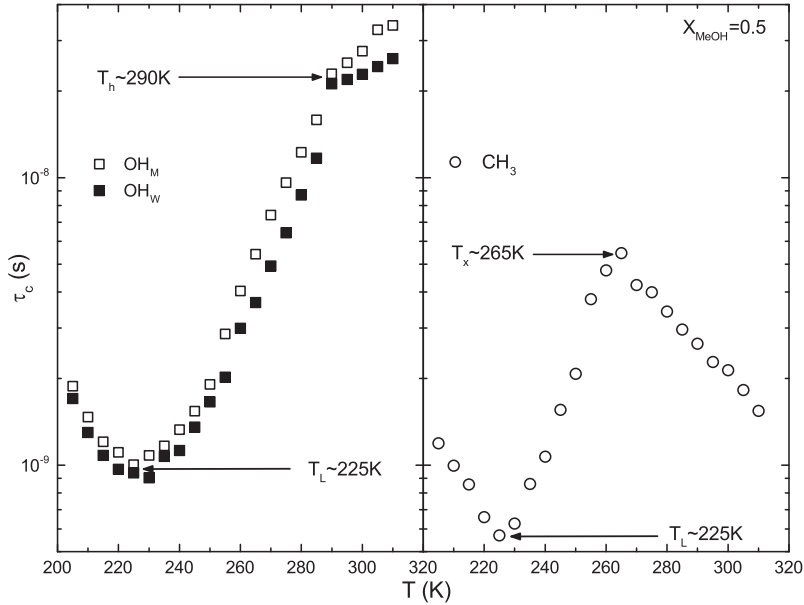


Fig. 4. – The average correlation time as a function of the temperature for hydroxyl protons of water and methanol (left panel) and for methyl protons of methanol (right panel) for the equimolar solution. Figure adapted from [21].

protons shows an inversion of its trend (right panel of fig. 4). For higher temperatures, and in particular for $T > 320$ K, the hydrogen bond lifetime is too small (less than picoseconds) to form stable structures and water behaves as a simple liquid [36, 37].

The τ_c of both moieties, instead, shows a minimum at 225 K where the correlations between water molecules reach their maximum value and the hydrogen bond network is completely developed [24, 38]. A smaller value in τ_c corresponds to faster correlation because of stronger interactions. The temperature T_L is also crucial for hydrated biological systems because above it the hydrogen bond network, formed by hydration water molecules, becomes softer due to the increase in the number of disordered water local structures [39, 40]. This phenomenon has been observed for many biological systems (*e.g.*, proteins, DNA, etc. [7, 41, 42]) and from our data we have the confirmation that this happens also for the smallest amphiphilic molecule. The hydrogen bond network, developed by water molecules, acts as a plasticizer of displacements strictly connected to the biological activity [43, 44].

4. – Conclusions

In conclusion, in our study we were able to identify the thermodynamic thresholds and their meaning in water/methanol solutions. As far as the concentration thresholds are concerned, they can be summarized as follows:

- $X_{MeOH} \sim 0.2$ is the concentration of minimum compressibility marking structural changes on the arrangement of water molecules induced by the hydrophobic effect.
- $X_{MeOH} \sim 0.4$ is the concentration of maximum slowing down for the dynamics of the solution, associated with the longest lifetime of mixed hydrogen bonded structures [45].
- $X_{MeOH} \sim 0.7$ is the threshold concentration of perturbation effects induced by water molecules on the methanol structures.

Note that these values are in agreement with those obtained by means of Terahertz Time-Domain Spectroscopy at 293 K [46] and Soft X-ray Absorption Spectroscopy at 298 K [47]. However, from our investigation these thresholds seem to soften and progressively disappear at the lowest temperatures.

Finally, we can list the temperature thresholds:

- $T_h \sim 290$ K is the threshold of the hydrophilic/hydrophobic competition, above which the hydrophobic force dominates over the hydrophilic interaction. This value is slightly dependent on the concentration being influenced by the amount of hydrophobic molecular groups present in the solution.
- $T_x \sim 265$ K is the onset temperature of the hydrophobic effect, and it does not depend on the molar fraction.
- $T_K \sim 245$ K marks the onset of segregation processes. Below this temperature, independent of the concentration, water and methanol molecules probe different chemical environments corresponding to those of pure compounds.
- $T_L \sim 225$ K is the temperature of the water dynamical crossover. For lower temperatures the hydrogen bonded network, characteristic of water, is completely developed and only a dynamics involving hopping processes, with a single characteristic time, is permitted.

At the highest temperatures, the so-called hydrophobic hydration favours the formation of long-lived water/methanol clusters. Upon cooling instead, the progressive increase of the hydrophilic interaction induces a rearrangement of hydrogen bonded structures and segregation processes with the formation of single-component aggregates.

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REFERENCES

- [1] MALLAMACE F., CORSARO C., MALLAMACE D., VASI C., VASI S. and STANLEY H. E., *J. Chem. Phys.*, **144** (2016) 064506.
- [2] BALL P., *Proc. Natl. Acad. Sci. USA*, **114** (2017) 13327.
- [3] RUPLEY J. A. and CARERI G., *Adv. Protein Chem.*, **41** (1991) 37.
- [4] BELLISSENT-FUNEL M. C., HASSANALI A., HAVENITH M., HENCHMAN R., POHL P., STERPONE F., VAN DER SPOEL D., XU Y. and GARCIA A. E., *Chem. Rev.*, **116** (2016) 7673.
- [5] GALLO, P., AMANN-WINKEL K., ANGELL C. A., ANISIMOV M. A., CAUPIN F., CHAKRAVARTY C., LASCARIS E., LOERTING T., PANAGIOTOPOULOS A. Z., RUSSO J. *et al.*, *Chem. Rev.*, **116** (2016) 7463.
- [6] CORSARO C., SPOOREN J., BRANCA C., LEONE N., BROCCIO M., KIM C., CHEN S.-H., STANLEY H. E. and MALLAMACE F., *J. Phys. Chem. B*, **112** (2008) 10449.
- [7] KÖHLER M. H., BARBOSA R. C., DA SILVA L. B. and BARBOSA M. C., *Phys. A Stat. Mech. Appl.*, **468** (2017) 733.
- [8] GIBSON R. E., *J. Am. Chem. Soc.*, **57** (1935) 1551.
- [9] FRANK H. S. and EVANS M. W., *J. Chem. Phys.*, **13** (1945) 507.
- [10] KOGA Y., *Mixing Schemes in Aqueous Mono-ols*, in *Solution Thermodynamics and its Application to Aqueous Solutions* (second edition), edited by FEDOR J. (Elsevier B. V.) 2017, pp. 115–197.
- [11] KAUZMANN W., *Adv. Protein Chem.*, **14** (1959) 1.
- [12] MALLAMACE F., CORSARO C., LONGO S., CHEN S.-H. and MALLAMACE D., *Colloids Surf. B: Biointerfaces*, **168** (2018) 193.
- [13] DIXIT S., CRAIN J., POON W. C. K., FINNEY J. L. and SOPER A. K., *Nature*, **416** (2002) 829.
- [14] DOUGAN L., BATES S. P., HARGREAVES R., FOX J. P., CRAIN J., FINNEY J. L., REAT V. and SOPER A. K., *J. Chem. Phys.*, **121** (2004) 6456.
- [15] YANO Y. F., *J. Colloid Interface Sci.*, **284** (2005) 255.
- [16] DOUGAN L., HARGREAVES R., BATES S. P., FINNEY J. L., REAT V., SOPER A. K. and CRAIN J., *J. Chem. Phys.*, **122** (2005) 174514.
- [17] SOPER A. K., DOUGAN L., CRAIN J. and FINNEY J. L., *J. Phys. Chem. B*, **110** (2006) 3472.
- [18] CORSARO C., MAISANO R., MALLAMACE D. and DUGO G., *Physica A*, **392** (2013) 596.
- [19] LAM R. K., SMITH J. W. and SAYKALLY R. J., *J. Chem. Phys.*, **144** (2016) 191103.
- [20] POŽAR M., KERASIDOU A., LOVRINČEVIĆ B., ZORANIĆ L., MIJAKOVIĆ M., PRIMORAC T., SOKOLIĆ F., TEBOUL V. and PERERA A., *J. Chem. Phys.*, **145** (2016) 144502.
- [21] CORSARO C., MALLAMACE F., VASI S., CHEN S.-H., STANLEY H. E. and MALLAMACE D., *Front. Phys.*, **13** (2018) 138201.
- [22] AUSTIN J. G., KURATA F. and SWIFT G. W., NASA Tech Briefs, 10274 (1968).
- [23] MALLAMACE F., BRANCA C., CORSARO C., LEONE N., SPOOREN J., STANLEY H. E. and CHEN S.-H., *J. Phys. Chem. B*, **114** (2010) 1870.
- [24] XU L., KUMAR P., BULDYREV S. V., CHEN S. H., POOLE P. H., SCIORTINO F. and STANLEY H. E., *Proc. Natl. Acad. Sci. USA*, **102** (2005) 16558.

- [25] NI Y. and SKINNER J. L., *J. Chem. Phys.*, **144** (2016) 214501.
- [26] CARPER W. R., *Concepts Magn. Reson. A*, **11** (1999) 51.
- [27] DE MARZIO M., CAMISASCA G., ROVERE M. and GALLO P., *J. Chem. Phys.*, **144** (2016) 074503.
- [28] CHONG S.-H., CHEN S.-H. and MALLAMACE F., *J. Phys.: Condens. Matter*, **21** (2009) 504101.
- [29] DEBENEDETTI P. G. and STILLINGER F. H., *Nature*, **410** (2001) 259.
- [30] YIP S., *Mol. Simul.*, **42** (2016) 1330.
- [31] ROYALL C. P. and WILLIAMS S. R., *Phys. Rep.*, **560** (2015) 1.
- [32] MALLAMACE F., CORSARO C., STANLEY H. E. and CHEN S.-H., *Eur. Phys. J. E*, **34** (2011) 94.
- [33] CORSARO C., MALLAMACE D., VASI S., CICERO N., DUGO G. and MALLAMACE F., *Nuovo Cimento C*, **39** (2016) 301.
- [34] GUO J. H., LUO Y., AUGUSTSSON A., KASHTANOV S., RUBENSSON J. E., SHUH D. K., ÅGREN H. and NORDGREN J., *Phys. Rev. Lett.*, **91** (2003) 157401.
- [35] GUEVARA-CARRION G., VRABEC J. and HASSE H., *J. Chem. Phys.*, **134** (2011) 074508.
- [36] MALLAMACE F., CORSARO C. and STANLEY H. E., *Sci. Rep.*, **2** (2012) 993.
- [37] MALLAMACE F., CORSARO C., MALLAMACE D., VASI C. and STANLEY H. E., *Faraday Discuss.*, **167** (2013) 95.
- [38] MALLAMACE F., CORSARO C., MALLAMACE D., VASI S., VASI C. and STANLEY H. E., *J. Chem. Phys.*, **141** (2014) 18C504.
- [39] GALLO P., AMANN-WINKEL K., ANGELL C. A., ANISIMOV M. A., CAUPIN F. *et al.*, *Chem. Rev.*, **116** (2016) 7463.
- [40] MALLAMACE F., CORSARO C., MALLAMACE D., VASI S. and STANLEY H. E., *J. Chem. Phys.*, **145** (2016) 214503.
- [41] CHEN S.-H., LIU L., CHU X., ZHANG Y., FRATINI E., BAGLIONI P., FARAONE A. and MAMONTOV E., *J. Chem. Phys.*, **125** (2006) 171103.
- [42] MALLAMACE F., BAGLIONI P., CORSARO C., CHEN S.-H., MALLAMACE D., VASI C. and STANLEY H. E., *J. Chem. Phys.*, **141** (2014) 165104.
- [43] DOSTER W. and SETTLES M., *Biochim. Biophys. Acta Proteins Proteom.*, **1749** (2005) 173.
- [44] MALLAMACE D., FAZIO E., MALLAMACE F. and CORSARO C., *Int. J. Mol. Sci.*, **19** (2018) 3825.
- [45] FERRARIO M., HAUGHNEY M., McDONALD I. R. and KLEIN M. L., *J. Chem. Phys.*, **93** (1990) 5156.
- [46] LI R., D'AGOSTINO C., MCGREGOR J., MANTLE M. D., ZEITLER J. A., and GLADDEN L. F., *J. Phys. Chem. B*, **118** (2014) 10156.
- [47] NAGASAKA M., MOCHIZUKI K., LELOUP V. and KOSUGI N., *J. Phys. Chem. B*, **118** (2014) 4388.